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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:32:20 ; Search time 2740 Seconds
(without alignments)
2018.078 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 190
Sequence: 1 MMNRQPPSKAMRASQMMTF.....HDGSLDLRSRSVQEGNPRA 190

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 2054640 seqs, 14551402878 residues

Word size: 4

Total number of hits satisfying chosen parameters: 2253933

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	190	100.0	1813	9 AK023655	AK023655 Homo sapi
3	190	100.0	1960	6 AX108538	AX108538 Sequence
4	190	100.0	2407	6 AX108534	AX108534 Sequence
5	190	100.0	2521	6 AX108536	AX108536 Sequence
6	190	100.0	2760	9 BC027602	BC027602 Homo sapi
7	135	71.1	2387	9 AK093944	AK093944 Homo sapi
8	126	66.3	2399	9 AK097718	AK097718 Homo sapi
9	59	31.1	220633	9 HU091321	U91321 Human Chrom
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11	35	18.4	164564	9 HUAC003108	AC003108 Human Chr
12	25	13.2	110000	2 AC124444_2	Continuation (3 of
13	18	9.5	623	10 MM0297000	AJ297000 Mus muscu
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17	10	5.3	4790	1 STYARABAD	M11047 S. typhimuri
18	10	5.3	20558	1 AE008698	AE008698 Salmonell
19	10	5.3	91692	2 CNG08C9G	AL732641 Oryza sat
20	10	5.3	150789	9 HS21F7	AL033375 Human DNA
21	10	5.3	163876	2 AC094128	AC094128 Rattus no
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RESULT 1

ALIGNMENTS

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AX108540
LOCUS: AX108540 1219 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 7 from Patent WO0123417.
ACCESSION AX108540
VERSION AX108540.1 GI:13923839
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS vinals y de Bassols,C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 7 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 346 a 260 c 275 g 338 t
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Pred. No.: 2.4e-189 Length: 1219
Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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QY 21 IlePheLeuLeuPhePheProSerPheThrglyValLeucystThreAlaIleThrIle 40
Db 64 ATCTTCTTCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC 123
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 124 TGGAGATTTGAAGCCTTACAGTGCAGTGGCCCTTTTCGAGGTGCTCTCTTCATTCAC 183
QY 61 SerIleTyrSerTrpIleAspThrIleSerThrArgProGlyTyrLeuTrpValValTrp 80
Db 184 TCCATCTACAGCTGATGATCAGACCCCTAAGTACACGGCTGCTGCTGCTGCTGCTG 243
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrIleValIleu 100
Db 244 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCCACCCCTCATTTGCTG 303
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
Db 304 ATCATCACCTATCTTACTGCGACATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363
QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 364 CATGAGCAGATCATTAATGAGGAGCAAGATAAATGTTCTGTAGAAATAATGATCAAG 423
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluIleArgArgVal 160
Db 424 CTGCAAGGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGGAGAGAGGTG 483
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
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QY 181 ArgSerValGlnGlyLysProArgAla 190
Db 544 AGATCAGTTCAAGAGGTAAATCCAAGGCC 573

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RESULT 2
LOCUS: AK023655 1813 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ13593 fis, clone PLACE1009493.
ACCESSION AK023655
VERSION AK023655.1 GI:10435644
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens placenta cDNA to mRNA, clone_11b.PLACE1
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosokiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahara,K., Masuho,Y., Niinomiya,K. and Iwayanagi,T.
NEDO human cDNA sequencing project
JOURNAL Unpublished
TITLE 2 (bases 1 to 1813)
REFERENCE Isogai,T. and Otsuki,T.
AUTHORS Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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BASE COUNT 489 a 400 c 405 g 519 t
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Db 571 TGGAGATTGAAGCCTTACAGCTGAGCTGTGGCCCTTTCGAGGCTCGCCCTTCATTCAC 630
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OY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 811 CATGAGCAGATCATTTAATGAGGGCAAGATAAATGTTCTGTATGAAAAATTGATCAAG 870
OY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
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OY 161 GluGlnGlnGlyPheLeuHisLeuGlyLysAspGlySerLeuAspLeuArgSerArg 180
Db 931 GAGCAACAAGCCTTTTGGCATTTGGGGGGAACATGATGCGAGTCTTGACATTGCGATCTAGA 990
OY 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 991 AGATCAGTTCAGAAGGTAATCCAAAGGCC 1020

RESULT 3
AX108538 1960 bp DNA linear PAT 30-APR-2001
AX108538
DEFINITION Sequence 5 from Patent WO0123417.
ACCESSION AX108538
VERSION AX108538.1 GI:13923838
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1960)
AUTHORS vinals y de Bassols,C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 5 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
source 1. 1960
location/Qualifiers
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB: 6

US-09-895-298a-83 (1-190) x AX108538 (1-1960)

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OY 161 GluGlnGlnGlyPheLeuHisLeuGlyLysAspGlySerLeuAspLeuArgSerArg 180
Db 1225 GAGCAACAAGCCTTTTGGCATTTGGGGGGAACATGATGCGAGTCTTGACATTGCGATCTAGA 1284
OY 181 ArgSerValGlnGluGlyAsnProArgAla 190
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RESULT 4
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AX108534
DEFINITION Sequence 1 from Patent WO0123417.
ACCESSION AX108534
VERSION AX108534.1 GI:13923834
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2407)
AUTHORS vinals y de Bassols,C.
TITLE Human tumor-associated lak-4p related polynucleotides and
polypeptides and their uses
JOURNAL Patent: WO 0123417-A 1 05-APR-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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location/Qualifiers
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DB: 6

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QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
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RESULT 5
AX108536

LOCUS AX108536 2521 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 3 from Patent WO0123417.
 ACCESSION AX108536
 VERSION AX108536.1 GI:13923835
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2521)
 AUTHORS Vinals y de Basols C.
 TITLE Human tumor-associated lak-4p related polynucleotides and
 polypeptides and their uses
 JOURNAL Patent: WO 0123417-A 3 05-APR-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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 source location/Qualifiers
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BASE COUNT 662 a 583 c 583 g 693 t
 ORIGIN

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QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
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 Db 1426 TGGAGATTGAAGCCTTCAGCTGACTGTGCCCCCTTTTCAGAGTCTGCCCTCTCTTCATTTCAC 1485
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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 Db 1486 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCCTGGCTAACCCTGTGGTGTGG 1545
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 |||||||
 Db 1546 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCTCACCCTCATCTGTGCTA 1605
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyValArgLysIleMetIleArgLeuLeu 120
 |||||||
 Db 1606 ATCATCACCCTATCTTACTGGCAGATCACAGAGGAAGAATTATGATTAAAGCTGCTC 1665
 QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
 |||||||
 Db 1666 CATGACAGATCATTAATGAGGGCAAAAGATAAATGTTCTCGATAGAAAAATGATCAAG 1725
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
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 Db 1726 CTGCAGAGATATGAGAGAAGCAAAACCCAGCTCATTCTTCTGGAAGAGAGAGGTG 1785
 QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
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 Db 1786 GAGCAACAAGGCTTTTTCATTTGGGGGAACATGATGCGAGCTTGTACTTGCATCTTACA 1845
 QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
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 Db 1846 AGATCAGTTCAAGAAGTAATCCAAGGGCC 1875

RESULT 6
 LOCUS BC027602 2760 bp mRNA linear PRI 01-MAY-2002
 DEFINITION Homo sapiens, Similar to RIKEN CDNA 4932443J08 gene, clone
 MGC:26648 IMAGE:4839111, mRNA, complete cds.
 ACCESSION BC027602
 VERSION BC027602.1 GI:20381190
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2760)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shriraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 34 Row: P Column: 13
 This clone was selected for full length sequencing because it

passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.

FEATURES

source

1. 2760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:26648 IMAGE:4839111"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

CDS

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/db_xref="GI:20381191"

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LSISIDVIDSQVSKNDQKQVLFSTLSNESMOTLHSLRCMGIDPSSHEV
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LNSISRAYRRKNSLSLISLISLMOKTIIIGKFGTSVLSYFNFLRLKFNISF
ILNFSFIIIPQTVAKNLTQFTGEEFTGVYFDRDWMYGGFTNSTIOHNSGASY
NMOLAYFTTGACLTCEFSLSFMAKFRNNFINPHYSGGITKLIFCDPTVTHEK
AVLKQKMLSTEIRNSELROENSKLTENOLTRFSYMWAVWVSTGVALAACAAVY
VLAERYNELKHSNPGAVLLPFEVSCINLAPCIYMERLVEYEMPREHYVLLI
RNIFLKISITIGLCYWNLTVALSGECCWETLIGODIYRLIMDFVSLVNSFLGEL
RRIIGMOLITSLGQEFIDFARNVELIYAQTLWIGIFCPLFIOMIMLFIYFYSK
NISLMMNFQPSKAMRASQOMTFIFLFPSTGVLTCLAITIRLKSADCPFGK
LPLFHSIYSWIDTLSTRPGYLMVWYIRNLIGSVHFEFLLITLIVLITLYWOITG
RKIMIRLHEQIINEGKMKLEIKLIKQMEKKANPSSVLERREVEQGFHLHGE
HDGSLDLRSRVSVOEGNPRA"

BASE COUNT 739 a 637 c 625 g 759 t
ORIGIN

Alignment Scores:

Pred. No.: 4.69e-189 Length: 2760
Score: 190.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-895-298a-83 (1-190) x BC027602 (1-2760)

OY 1 MetetAsnPhenGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrpPhe 20
DB 1923 ATGATGAATTCACAGCTCCGAGAAAGCCTGGCGGCTCAGATGATGACTTCTTC 1982
OY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
DB 1983 ATCTTCTGCTCTTTTCCATCTTCACCGGGGCTTGTGTGACCCCTGGCCATCACCATC 2042
OY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
DB 2043 TGGAGATTGAAGCCTTCAGCTGTGCTGCTTTCGAGGCTGCTCCTTCAATTCAC 2102
OY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValTrp 80
DB 2103 TCCATCTACAGCTGGATGACACCTTAAGTACACGGCTGCTACCTGTGGGTTGTTGG 2162
OY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
DB 2163 ATCATCGGAACCTCATGGAAGTGCACCTTCTTTCATCCACCCCATGTCGCTA 2222
OY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyValArgLysIleMetIleArgLeu 120
DB 2223 ATCATCACCTATCTTACTGGACATCACAGAGGGAAGATATATGATAAAGGCTGCTC 2282
OY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
DB 2283 CATGACGATCATTAATGAGGGAAGATAAATGTTCTGTATGAAAAATGTATCAAG 2342
OY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnVal 160

DB 2343 CTGCAGATATGAGAGAAAGCAAAACCCAGCTGTTCTGTGAAAAGAGAGAGGTG 2402
OY 161 GlnGlnGlnGlyPheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArg 180
DB 2403 GAGCAACAAGCTTTTTCGATTTGGGGGAGATGATGCGAGCTTGTGCGATCTAGA 2462
OY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
DB 2463 AGATCAGTTCAAGAAAGTATCAAGGCGC 2492

RESULT 7

AK093944 2387 bp mRNA linear PRI 15-JUL-2002
LOCUS
DEFINITION Homo sapiens cDNA FLJ36625 fts, clone TRACH2017368, weakly similar to Homo sapiens mRNA for LAR-4p.

ACCESSION AK093944
VERSION AK093944.1 GI:21752906
KEYWORDS oligo capping; fts (full insert sequence).
SOURCE Homo sapiens trachea cDNA to mRNA, clone_lib:TRACH2
clone:TRACH2017368.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Salto, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Magatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project

TITLE Unpublished
JOURNAL 2 (bases 1 to 2387)
REFERENCE Isogai, T. and Yamamoto, J.
AUTHORS Direct Submission
TITLE Submitted (04-JUL-2002) Takao Isogai, Fij Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
JOURNAL (E-mail:genomices@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

source

1. 2387
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TRACH2017368"
/tissue_type="trachea"
/clone_lib="TRACH2"
/note="cloning vector: pME18SFL3"

BASE COUNT 624 a 549 c 543 g 671 t
ORIGIN

Alignment Scores:

Pred. No.: 1.96e-131 Length: 2387
Score: 135.00 Matches: 189
Percent Similarity: 98.95% Conservative: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 71.05% Indels: 2
DB: 9 Gaps: 0

US-09-895-298a-83 (1-190) x AK093944 (1-2387)

QY 1 MetMetasnpheglnpProserLysAlaTrpArgAlaSerGlnMetMetThrphe 20
 Db 1025 ATGATGATATTCACGCTCCGAGCAAGCGCTGGCGGCTCCAGATGATGACTTCTTC 1084
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrile 40
 Db 1085 ATCTTCTGCTCTTTTCCCAATCTTCACCGGGGCTTGTGTGCACCTGGCCATCACCATC 1144
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 Db 1145 TGGAGATTGAAGCCTTCAGCTGAGTGCCTTTTCGAGAGTCTGCTCTTCATTTCAC 1204
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
 Db 1205 TCCATCTACAGCTGCATCGACACCTTAAGTACACGGCTGCTACCTGTGGTGTGG 1264
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 Db 1265 ATCTATCGAACCCTCATTTGAGAGTGCACCTTTTTCATCTCCTCACTTGTGCTA 1324
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgGlyIleMetIleArgLeuLeu 120
 Db 1325 ATCATCACCCTATCTTACTGTGCAGATCACAGAGGAGAGATATGATTAAGCTGCTC 1384
 QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGlu-LysIleIlely 140
 Db 1385 CATGACGAGATCATTAATGAGGCGCAAGATTAATGTTCTGTATAGG-AAATTTGATCAA 1443
 QY 140 sleuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
 Db 1444 GCTGACGAGATATGAGAGAGAGCAAAACCCAGCTACTTGTCTGGAAGAGAGAGGCT 1503
 QY 160 IGLuGlnGlnGlyPheLeuHisIleGlyGluHisAspGlySerLeuAspLeuArgSerAr 180
 Db 1504 GGAGCAACAAGGCTTTTTCATTTGGGGGGAACATGATGACATGCTTGTGCGATCTAG 1563
 QY 180 GArgSerValGlnGluGlyAsnProArgAla 190
 Db 1564 AAGATCAGTCAAGAAGGTATCAAGGCC 1594
 RESULT 8
 AK097718 2399 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens cDNA FLJ40399 fis, clone TESTI2037081, weakly similar
 ACCESSION AK097718
 VERSION AK097718.1 GI:21757573
 KEYWORDS oligo capping; fis (full insert sequence)
 SOURCE Homo sapiens testis cDNA to mRNA, clone_11b:TESTI2
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
 Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R.,
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
 Kawal, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
 Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B.,
 Suzuki, Y., Sugano, S., Nagahari, K., Masuno, Y., Nagai, K. and
 Isogai, T.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE
 AUTHORS Isogai, T. and Yamamoto, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, Flj Project(HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology (RAB); cDNA library

FEATURES
 source
 1. 2399
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TESTI2037081"
 /tissue_type="testis"
 /clone_lib="TESTI2"
 /note="cloning vector: pME18SFL3"
 BASE COUNT 610 a 591 c 528 g 670 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,37e-122 Length: 2399
 Score: 126.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 66.32% Indels: 0
 DB: Gaps: 0
 US-09-895-298a-83 (1-190) x AK097718 (1-2399)
 QY 1 MetMetasnpheglnpProserLysAlaTrpArgAlaSerGlnMetMetThrphe 20
 Db 1933 ATGATGATATTCACGCTCCGAGCAAGCGCTGGCGGCTCCAGATGATGACTTCTTC 1992
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrile 40
 Db 1993 ATCTTCTGCTCTTTTCCCAATCTTCACCGGGGCTTGTGTGCACCTGGCCATCACCATC 2052
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 Db 2053 TGGAGATTGAAGCCTTCAGCTGAGTGCCTTTTCGAGGTCTGCCCTCTTCATTTCAC 2112
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
 Db 2113 TCCATCTACAGCTGCATCGACACCTTAAGTACACGGCTGCTACCTGTGGTGTGG 2172
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 Db 2173 ATCTATCGAACCCTCATTTGAGAGTGCACCTTTTTCATCTCCTCACTTGTGCTA 2232
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgGlyIleMetIleArgLeuLeu 120
 Db 2233 ATCATCACCCTATCTTACTGTGCAGATCACAGAGGAGAGATTAATTAAGCTGCTC 2292
 QY 121 HisGluGlnIleIleAsn 126
 Db 2293 CATGACGAGATCATTAAT 2310
 RESULT 9
 HUU91321 220633 bp DNA linear PRI 10-JAN-2000
 LOCUS Human Chromosome 16 BAC clone CIT9875K-A-363B6, complete sequence.
 ACCESSION U91321
 VERSION U91321.1 GI:2951946
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Loftus, B.J., Kim, D.J., Sneddon, V.P., Kalush, F., Brandon, R.,
 Fuhmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L.,
 Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S.,
 Eichler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D.
 TITLE Genome duplications and other features in 12 Mb of DNA sequence
 from human chromosome 16p and 16q
 JOURNAL Genomics 60 (3), 295-308 (1999)


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MEDLINE      99425270
REFERENCE    10493829
AUTHORS      2 (bases 1 to 220633)
TITLE        Adams,M.D., Loftus,B.J., Phillips,C.A., Zhou,L., Brandon,R.,
JOURNAL      Fuhrmann,J. and Venter,J.C.
REFERENCE    Direct Submission
AUTHORS      Submitted (04-MAR-1997) The Institute for Genomic Research, 9712
JOURNAL      Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    3 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L. and Lombard,M.
TITLE        Direct Submission
JOURNAL      Submitted (21-MAY-1997)
AUTHORS      4 (bases 1 to 220633)
REFERENCE    Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
JOURNAL      Venter,J.C.
REFERENCE    Direct Submission
AUTHORS      Submitted (19-AUG-1997) The Institute for Genomic Research, 9712
JOURNAL      Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    5 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
JOURNAL      Venter,J.C.
REFERENCE    Direct Submission
AUTHORS      Submitted (22-AUG-1997) The Institute for Genomic Research, 9712
JOURNAL      Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    6 (bases 1 to 220633)
AUTHORS      Adams,M.D.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-1998) The Institute for Genomic Research, 9712
AUTHORS      Medical Center Dr., Rockville, MD 20850, USA
COMMENT      On Mar 11, 1998 this sequence version replaced gi:2335062.
              BAC clone C1987SK-363E6 is located in band 16p13.1 of chromosome
              16. Genes were identified by a combination of five methods:
              XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov),
              GeneFinder (available by anonymous ftp from
              colineu.washington.edu), GENSCAN (available using the e-mail server
              at gensec.genomic.stanford.edu), searches of the ESR database at
              TIGR (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a
              peptide database. Repeats were identified using RepeatMasker (Smit,
              A.F.A. and Green, P. unpublished,
              http://ftp.genome.washington.edu/rm/RepeatMasker.html).
FEATURES
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              /gene="363E6.1"
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              TIMAPSAWFLF"
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              /translation="MRQTRDVTALTRPMSLSHTGDKPRYDTFWKHIFVAMDL
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BASE COUNT   61048 a 48977 c 49108 g 61449 t 51 others

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ORIGIN
Alignment Scores:
Pred. No.: 3 89e-50
Score: 59.00
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Best Local Similarity: 100.00%
Query Match: 31.05%
DB: 9
Gaps: 0
US-09-895-298A-83 (1-190) x HUU91321 (1-220633)
QY 42 ArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSer 61
DB 204866 AGATTGAGCCTTCACCTGACCTGTGGCCCTTTTCGAGGCTGCTCTCTTCATTCACCTCC 204925
QY 62 IleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIle 81
DB 204926 ATCTACAGCTGATCGACACCCCTAGTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 204985
QY 82 TyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
DB 204986 TATCGGAACCTCATTTGGAAGTGTGCACCTCTTTTCATCTACCCCTCATTTGTGCTG 205042
RESULT 10
AC130456 223280 bp DNA linear HTG 10-AUG-2002
LOCUS Homo sapiens chromosome 16 clone CTA-363E6, WORKING DRAFT SEQUENCE,
DEFINITION 5 unordered pieces.
AC130456
AC130456
VERSION AC130456.1 GI:22203229
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 223280)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 223280)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
          Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
          Center: Joint Genome Institute
          Center Code: JGI
          Web site: http://www.jgi.doe.gov
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          Project Information
          Center Project Name: 2773242
          Center clone name: C1978SKA_363E6
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          Summary Statistics
          Consensus quality: 221100 bases at least Q40
          Consensus quality: 222027 bases at least Q30
          Consensus quality: 222494 bases at least Q20
          Estimated insert size: 220633; agarose-fp estimation
          Estimated insert size: 222880; sum-of-contigs estimation
          Quality coverage: 10.71 in Q20 bases; sum-of-contigs estimation
          Quality coverage: 10.81 in Q20 bases; sum-of-contigs estimation.
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 5 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          * 1 1261: contig of 1261 bp in length
          * 1262 1361: gap of unknown length
          * 1362 2690: contig of 1329 bp in length

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FEATURES
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 1. 223280
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 /db_xref="taxon:9606"
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 ORIGIN

Alignment Scores:
 Pred. No.: 3.93e-50 Length: 223280
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 164564)
 Loftus,B.J., Kim,U.J., Shedd,V.P., Kalush,F., Brandon,R.,
 Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
 Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
 Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
 Genome duplications and other features in 12 Mb of DNA sequence
 from human chromosome 16p and 16q

TITLE
 JOURNAL Genomics 60 (3), 295-308 (1999)
 MEDLINE 99425270
 PUBMED 10493829

REFERENCE
 2 (bases 1 to 164564)

ADITHORS
 Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J.,
 Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
 Human Chromosome 16 BAC clone C1987SK-327024
 Unpublished

TITLE
 JOURNAL 3 (bases 1 to 164564)
 ADITHORS
 Adams,M.D. and Loftus,B.J.
 Direct Submission
 Submitted (19-NOV-1997) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, Email:
 b1loftus@tigr.org

REFERENCE
 4 (bases 1 to 164564)
 ADITHORS
 Adams,M.D.
 Direct Submission

JOURNAL
 Submitted (05-FEB-1998) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 5 (bases 1 to 164564)
 ADITHORS
 Adams,M.D. and Loftus,B.J.
 Direct Submission
 Submitted (17-MAR-1998) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Feb 5, 1998 this sequence version replaced gi:2827780.
 Address all correspondence to: Mark Adams The Institute for Genomic
 Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail
 address: mdamas@tigr.org. The orientation of the sequence is from
 SP6 end to 7' end. Genes were identified by a combination of five
 methods including: XGRAIL (available by anonymous ftp from
 arthur.epm.ornl.gov), Genefinder (Phil Green, University of
 Washington), Genscan (Chris Burge,
 http://gnomic.stanford.edu/chris/GENSCANW.html) searches of the
 complete sequence against a peptide database, and the Human gene
 Index database at TIGR (http://www.tigr.org/cdb/hgl/hgl.html).
 Genes without peptide homology having spliced EST hits are termed
 'Unknown gene product'. Genes encoding tRNAs are predicted by
 tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).

FEATURES
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misc_feature

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mRNA

CDS

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ALIMOV. VIMENLIN.
SOURCE house mouse.

McCaldin, M., McEwan, P., McEneaney, K., McNeely, R., Melis, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

TITLE
JOURNAL

COMMENT

Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Rhoman, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L13918

Center clone name: 35_B_17

* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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